

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539,946
Source: P4/10
Date Processed by STIC: 6/30/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2005

PATENT APPLICATION: US/10/539,946

TIME: 09:01:28

Input Set : A:\pct-kr05-00457.txt

Output Set: N:\CRF4\06302005\J539946.raw

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1 <110> APPLICANT: MEDEXGEN CO., LTD
3 <120> TITLE OF INVENTION: Pharmaceutical Composition for treatment of Transplantation
4   Rejection comprising Concatameric Immunoadhesin
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/539,946
C--> 6 <141> CURRENT FILING DATE: 2005-06-16
W--> 0 <130> FILE REFERENCE:
      6 <160> NUMBER OF SEQ ID NOS: 26
      8 <170> SOFTWARE: KopatentIn 1.71
10 <210> SEQ ID NO: 1
11 <211> LENGTH: 31
12 <212> TYPE: DNA
13 <213> ORGANISM: Artificial Sequence
15 <220> FEATURE:
16 <223> OTHER INFORMATION: primer, oligo-LAG3-F-EcoRI
19 <400> SEQUENCE: 1
20 ggaattcatg tgggaggctc agttcctggg c                               31
23 <210> SEQ ID NO: 2
24 <211> LENGTH: 28
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: primer, oligo-LAG3-R-5P
32 <400> SEQUENCE: 2
33 agtgaggta tacatgatgg agacgttg                                     28
36 <210> SEQ ID NO: 3
37 <211> LENGTH: 21
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: primer, oligo-LAG3-F-5P
45 <400> SEQUENCE: 3
46 ctccagccag gggctgaggt c                                           21
49 <210> SEQ ID NO: 4
50 <211> LENGTH: 30
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
54 <220> FEATURE:
55 <223> OTHER INFORMATION: primer, oligo-LAG3-R-SpeI
58 <400> SEQUENCE: 4
59 gactagttgg gggctccaga cccagaacag                                   30
62 <210> SEQ ID NO: 5
63 <211> LENGTH: 28
64 <212> TYPE: DNA

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65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: primer, hIgG-F-SpeI
71 <400> SEQUENCE: 5
72 gagtagtgca gagcccaaatt cttgtgac 28
75 <210> SEQ ID NO: 6
76 <211> LENGTH: 34
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: primer, hIgG-R-XbaI
84 <400> SEQUENCE: 6
85 gctctagagc tcatttacct ggagacaggg agag 34
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 1503
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
93 <220> FEATURE:
94 <221> NAME/KEY: sig_peptide
95 <222> LOCATION: (1)..(66)
97 <220> FEATURE:
98 <221> NAME/KEY: CDS
99 <222> LOCATION: (1)..(1500)
100 <223> OTHER INFORMATION: LAG3/Fc
103 <400> SEQUENCE: 7
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105 Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
106 1 5 10 15
108 gtg gct cca gtg aag cct ctc cag cca ggg gct gag gtc ccg gtg gtg 96
109 Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
110 20 25 30
112 tgg gcc cag gag ggg gct cct gcc cag ctc ccc tgc agc ccc aca atc 144
113 Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
114 35 40 45
116 ccc ctc cag gat ctc agc ctt ctg cga aga gca ggg gtc act tgg cag 192
117 Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
118 50 55 60
120 cat cag cca gac agt ggc ccg ccc gct gcc gcc ccc ggc cat ccc ctg 240
121 His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
122 65 70 75 80
124 gcc ccc ggc cct cac ccg gcg gcg ccc tcc tcc tgg ggg ccc agg ccc 288
125 Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
126 85 90 95
128 cgc cgc tac acg gtg ctg agc gtg ggt ccc gga ggc ctg cgc agc ggg 336
129 Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
130 100 105 110
132 agg ctg ccc ctg cag ccc cgc gtc cag ctg gat gag cgc ggc cgg cag 384
133 Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
134 115 120 125

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136	cgc	ggg	gac	ttc	tcg	cta	tgg	ctg	cgc	cca	gcc	cgg	cgc	gcg	gac	gcc	432
137	Arg	Gly	Asp	Phe	Ser	Leu	Trp	Leu	Arg	Pro	Ala	Arg	Arg	Ala	Asp	Ala	
138		130					135					140					
140	ggc	gag	tac	cgc	gcc	gcg	gtg	cac	ctc	agg	gac	cgc	gcc	ctc	tcc	tgc	480
141	Gly	Glu	Tyr	Arg	Ala	Ala	Val	His	Leu	Arg	Asp	Arg	Ala	Leu	Ser	Cys	
142	145					150					155					160	
144	cgc	ctc	cgt	ctg	cgc	ctg	ggc	cag	gcc	tcg	atg	act	gcc	agc	ccc	cca	528
145	Arg	Leu	Arg	Leu	Arg	Leu	Gly	Gln	Ala	Ser	Met	Thr	Ala	Ser	Pro	Pro	
146					165					170						175	
148	gga	tct	ctc	aga	gcc	tcc	gac	tgg	gtc	att	ttg	aac	tgc	tcc	ttc	agc	576
149	Gly	Ser	Leu	Arg	Ala	Ser	Asp	Trp	Val	Ile	Leu	Asn	Cys	Ser	Phe	Ser	
150				180						185					190		
152	cgc	cct	gac	cgc	cca	gcc	tct	gtg	cat	tgg	ttc	cgg	aac	cgg	ggc	cag	624
153	Arg	Pro	Asp	Arg	Pro	Ala	Ser	Val	His	Trp	Phe	Arg	Asn	Arg	Gly	Gln	
154			195					200					205				
156	ggc	cga	gtc	cct	gtc	cgg	gag	tcc	ccc	cat	cac	cac	tta	gcg	gaa	agc	672
157	Gly	Arg	Val	Pro	Val	Arg	Glu	Ser	Pro	His	His	His	Leu	Ala	Glu	Ser	
158		210				215						220					
160	ttc	ctc	ttc	ctg	ccc	caa	gtc	agc	ccc	atg	gac	tct	ggg	ccc	tgg	ggc	720
161	Phe	Leu	Phe	Leu	Pro	Gln	Val	Ser	Pro	Met	Asp	Ser	Gly	Pro	Trp	Gly	
162	225				230					235						240	
164	tgc	atc	ctc	acc	tac	aga	gat	ggc	ttc	aac	gtc	tcc	atc	atg	tat	aac	768
165	Cys	Ile	Leu	Thr	Tyr	Arg	Asp	Gly	Phe	Asn	Val	Ser	Ile	Met	Tyr	Asn	
166				245						250					255		
168	ctc	act	gtt	ctg	ggt	ctg	gag	ccc	cca	act	agt	gca	gag	ccc	aaa	tct	816
169	Leu	Thr	Val	Leu	Gly	Leu	Glu	Pro	Pro	Thr	Ser	Ala	Glu	Pro	Lys	Ser	
170			260							265					270		
172	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	864
173	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
174			275					280						285			
176	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	912
177	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
178		290				295						300					
180	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	960
181	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
182	305				310					315						320	
184	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	1008
185	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
186				325						330					335		
188	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	1056
189	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
190			340							345					350		
192	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	1104
193	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
194		355				360							365				
196	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	1152
197	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
198		370				375						380					
200	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	1200

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201 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
202 385          390          395          400
204 gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc      1248
205 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
206          405          410          415
208 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      1296
209 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
210          420          425          430
212 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      1344
213 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
214          435          440          445
216 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc      1392
217 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
218          450          455          460
220 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      1440
221 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
222 465          470          475          480
224 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      1488
225 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
226          485          490          495
228 tcc ccg ggt aaa          tga      1503
229 Ser Pro Gly Lys
230          500
233 <210> SEQ ID NO: 8
234 <211> LENGTH: 500
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 8
239 Met Trp Glu Ala Gln Phe Leu Gly Leu Leu Phe Leu Gln Pro Leu Trp
240 1          5          10          15
242 Val Ala Pro Val Lys Pro Leu Gln Pro Gly Ala Glu Val Pro Val Val
243          20          25          30
245 Trp Ala Gln Glu Gly Ala Pro Ala Gln Leu Pro Cys Ser Pro Thr Ile
246          35          40          45
248 Pro Leu Gln Asp Leu Ser Leu Leu Arg Arg Ala Gly Val Thr Trp Gln
249          50          55          60
251 His Gln Pro Asp Ser Gly Pro Pro Ala Ala Ala Pro Gly His Pro Leu
252 65          70          75          80
254 Ala Pro Gly Pro His Pro Ala Ala Pro Ser Ser Trp Gly Pro Arg Pro
255          85          90          95
257 Arg Arg Tyr Thr Val Leu Ser Val Gly Pro Gly Gly Leu Arg Ser Gly
258          100          105          110
260 Arg Leu Pro Leu Gln Pro Arg Val Gln Leu Asp Glu Arg Gly Arg Gln
261          115          120          125
263 Arg Gly Asp Phe Ser Leu Trp Leu Arg Pro Ala Arg Arg Ala Asp Ala
264          130          135          140
266 Gly Glu Tyr Arg Ala Ala Val His Leu Arg Asp Arg Ala Leu Ser Cys
267 145          150          155          160
269 Arg Leu Arg Leu Arg Leu Gly Gln Ala Ser Met Thr Ala Ser Pro Pro

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```

270          165          170          175
272 Gly Ser Leu Arg Ala Ser Asp Trp Val Ile Leu Asn Cys Ser Phe Ser
273          180          185          190
275 Arg Pro Asp Arg Pro Ala Ser Val His Trp Phe Arg Asn Arg Gly Gln
276          195          200          205
278 Gly Arg Val Pro Val Arg Glu Ser Pro His His His Leu Ala Glu Ser
279          210          215          220
281 Phe Leu Phe Leu Pro Gln Val Ser Pro Met Asp Ser Gly Pro Trp Gly
282 225          230          235          240
284 Cys Ile Leu Thr Tyr Arg Asp Gly Phe Asn Val Ser Ile Met Tyr Asn
285          245          250          255
287 Leu Thr Val Leu Gly Leu Glu Pro Pro Thr Ser Ala Glu Pro Lys Ser
288          260          265          270
290 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
291          275          280          285
293 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
294          290          295          300
296 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
297 305          310          315          320
299 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
300          325          330          335
302 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
303          340          345          350
305 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
306          355          360          365
308 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
309          370          375          380
311 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
312 385          390          395          400
314 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
315          405          410          415
317 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
318          420          425          430
320 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
321          435          440          445
323 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
324          450          455          460
326 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
327 465          470          475          480
329 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
330          485          490          495
332 Ser Pro Gly Lys
333          500
336 <210> SEQ ID NO: 9
337 <211> LENGTH: 2211
338 <212> TYPE: DNA
339 <213> ORGANISM: Homo sapiens
341 <220> FEATURE:
342 <221> NAME/KEY: sig_peptide

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,946

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Input Set : A:\pct-kr05-00457.txt

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L:6 M:270 C: Current Application Number differs, Replaced Current Application No

L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE